CLAIMS

What is claimed is:

1. A method of creating a peptide database, said method comprising:
providing a first source of peptides;
screening a peptide to determine the activity of the peptide;
analyzing the results;
characterizing a physical, chemical, or biological property of the peptides;
recording in a peptide database the characteristics of all peptides;
recording in the peptide database results of said analyzing the peptides, thereby generating a database or part of a database of peptides.

2. The method according to claim 1, wherein said peptides are related to gonadotropin.

3. The method according to claim 1, wherein said peptides are between three and four amino acids in length.

4. The method according to claim 1, wherein said step of characterizing a physical, chemical, or biological property of the peptides comprises determining an effect of the peptide on nitrous oxide production in a cell.

5. The method according to claim 1, wherein said step of characterizing a physical, chemical, or biological property of the peptides comprises conducting a glucose tolerance test.

6. The method for creating a peptide database according to claim 1, further comprising aligning a sequence of a subset of the peptides.

7. The method for creating a peptide database according to claim 6, further comprising determining a consensus sequence.

8. The method for creating a peptide database according to claim 6, further comprising determining positional information.

9. The method according to claim 6, wherein the peptides are from two different species.

10. The method according to claim 1, wherein said peptides are related to human chorionic gonadotropin.

11. The method according to claim 1, wherein analyzing the peptides comprises analyzing an anti-shock effect.

12. The method according to claim 1, wherein analyzing the peptides comprises analyzing TNF-α.

13. The method according to claim 1, wherein analyzing the peptides comprises analyzing an affect of a peptide on angiogenesis.

14. The method according to claim 1, wherein analyzing the peptides comprises analyzing a condition associated with a dysfunctional LDL receptor.

15. The method according to claim 1, wherein analyzing the peptides comprises analyzing the affect of the peptide on at least one inflammatory mediator selected from the group consisting of IL-1-α, IL-1-β, IL-6, TNF-α, LIF, IFN-γ, OSM, CNTF, GM-CSF, IL-11, IL-12, IL-17, IL-18 and IL-8.

16. The method according to claim 1, wherein said peptide database further comprises annotational information relating to said polynucleotide sequences

17. The method according to claim 16, wherein said annotational information comprises at least one of origin, source, features and references for said peptides.

18. The method according to claim 1, further comprising searching the peptide database for a peptide having specified characteristics.

19. The method according to claim 18, wherein searching the peptide database is performed from a remote location.

20. The method according to claim 1, further comprising identifying one or more proteins having immunoregulatory activity and/or gene regulatory activity.

21. The method according to claim 1, wherein screening a peptide to determine the activity of the peptide comprises screening a peptide array.

22. The method according to claim 1, wherein said peptides are related to Beta-catenin.

23. The method according to claim 1, wherein said peptides are related to C-reactive protein.

24. The method according to claim 1, wherein said peptides are related to matrix metalloproteinase-2.

25. The method according to claim 1, wherein said peptides are related to Bruton's tyrosine kinase.

26. A method implemented in a computer system for presenting biomolecular sequence data, said method comprising:

retrieving protein characteristic data from a database in response to a user query; and

graphically depicting elements of the protein characteristic data in a user interface for said computer system, wherein said graphical depiction comprises at least one panel graphically depicting peptide sequence or composition information.

27. A method of producing a pharmaceutical, said method comprising:

determining the identity of a compound that modulates an activity selected from the group consisting of development of the systemic inflammatory response, release of other inflammatory mediators, regulation of members of the nuclear factor-κB family, accentuation or protection from sepsis, nitrate production, nitric oxide production, glucose tolerance and combinations thereof;

conducting therapeutic profiling of the compound for efficacy and toxicity in animals; and

formulating a pharmaceutical preparation including one or more compounds identified as having an acceptable therapeutic profile.

28. The method according to claim 27, further comprising establishing a distribution system for distributing the pharmaceutical preparation.

29. The method according to claim 28, further comprising establishing a sales group for marketing the pharmaceutical preparation.

30. The method according to claim 27, wherein determining the identity of a compound comprises searching a peptide database.

31. An improvement in a method of screening a candidate compound for biological activity by screening the compound in a cell line, the improvement comprising:

screening said candidate compound in a cell line wherein said cell line has been contacted with at least one exogenously added biologically active peptide having gene regulatory activity.

32. The method according to claim 31, wherein the at least one exogenously added biologically active peptide is selected from the list of peptides present in Table 1, Table 2, Table 3, Table 4, Table 5, or Table 6.

33. A method of identifying biologically active peptide fragments comprising:

identifying a protein that is subsequently cleaved in a subject's body by a peptidase to form a peptide having an activity as well as peptide fragments, and

analyzing said peptide fragments for biological activity.

34. The method according to claim 33 wherein the biological activity is gene regulatory activity.

35. The method according to claim 33, wherein the protein is hCG.

36. The method according to claim 33, wherein the biological activity of the peptide fragments is different than the activity of the activity of the peptide.

37. The method according to claim 33, wherein the protein is Beta-catenin.

38. The method according to claim 33, wherein the protein is C-reactive protein.

39. The method according to claim 33, wherein the protein is matrix metalloproteinase-2.

40. The method according to claim 33, wherein the protein is Bruton's tyrosine kinase.

41. The method according to claim 33, wherein the peptide fragments are timers or tetramers.

42. The method according to claim 41, further comprising entering data obtained from analyzing said peptide fragments for biological activity into a database.

43. The method according to claim 33 wherein biological activity is determined by contacting a cell or cell culture with a peptide fragment and determining the gene expression profile of said cell or cell culture.

44. The method according to claim 43, wherein said expression profile is compared with the expression profile of a control cell or cell culture not having been contacted with said peptide fragment.

45. The method according to claim 43, further comprising generating a database describing genes up-regulated or down-regulated by said peptide fragment.

46. A database generated by a method according to claim 45.